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RAW SEQUENCE LISTING

DATE: 06/26/2001

PATENT APPLICATION: US/09/848,164

TIME: 15:15:09

Input Set : N:\Cr3\RULE60\09848164.txt

Output Set: N:\CRF3\06262001\I848164.raw

#2

SEQUENCE LISTING

ENTERED

4 (1) GENERAL INFORMATION:

6 (i) APPLICANT: Rhode, Peter R.

7 Jiao, Jin-An

8 Burkhardt, Martin

9 Wong, Hing

11 (ii) TITLE OF INVENTION: MHC COMPLEXES AND USES THEREOF

13 (iii) NUMBER OF SEQUENCES: 124

15 (iv) CORRESPONDENCE ADDRESS:

16 (A) ADDRESSEE: Dade International, Inc.

17 (B) STREET: 1717 Deerfield Road

18 (C) CITY: Deerfield

19 (D) STATE: Illinois

20 (E) COUNTRY: USA

21 (F) ZIP: 60015

23 (v) COMPUTER READABLE FORM:

24 (A) MEDIUM TYPE: Floppy disk

25 (B) COMPUTER: IBM PC compatible

26 (C) OPERATING SYSTEM: PC-DOS/MS-DOS

27 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30

29 (vi) CURRENT APPLICATION DATA:

C--> 30 (A) APPLICATION NUMBER: US/09/848,164

C--> 31 (B) FILING DATE: 03-May-2001

32 (C) CLASSIFICATION:

42 (vii) PRIOR APPLICATION DATA:

35 (A) APPLICATION NUMBER: 09/067,615

36 (B) FILING DATE:

39 (A) APPLICATION NUMBER: US 08/382,454

40 (B) FILING DATE: 01-FEB-1995

43 (A) APPLICATION NUMBER: US 08/283,302

44 (B) FILING DATE: 29-JUL-1994

46 (viii) ATTORNEY/AGENT INFORMATION:

47 (A) NAME: Pearson, Louise S.

48 (B) REGISTRATION NUMBER: 32,369

49 (C) REFERENCE/DOCKET NUMBER: STR-4665-CIP2

51 (ix) TELECOMMUNICATION INFORMATION:

52 (A) TELEPHONE: (708) 267-5300

53 (B) TELEFAX: (708) 267-5376

56 (2) INFORMATION FOR SEQ ID NO: 1:

58 (i) SEQUENCE CHARACTERISTICS:

59 (A) LENGTH: 10 amino acids

60 (B) TYPE: amino acid

61 (C) STRANDEDNESS: unknown

62 (D) TOPOLOGY: unknown

64 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

66 Ala Ser Gly Gly Gly Gly Ser Gly Gly Gly

67 1 5 10

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70 (2) INFORMATION FOR SEQ ID NO: 2:
71     (i) SEQUENCE CHARACTERISTICS:
72         (A) LENGTH: 8 base pairs
73         (B) TYPE: nucleic acid
74         (C) STRANDEDNESS: unknown
75         (D) TOPOLOGY: unknown
76     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
77     CCACCATG
78
83 (2) INFORMATION FOR SEQ ID NO: 3:
84     (i) SEQUENCE CHARACTERISTICS:
85         (A) LENGTH: 18 amino acids
86         (B) TYPE: amino acid
87         (C) STRANDEDNESS: unknown
88         (D) TOPOLOGY: unknown
89     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
90     Ser Ile Ser Gln Ala Val His Ala Ala His Ala Glu Ile Asn Glu Ala
91     1             5             10             15
92     Gly Arg
93
99 (2) INFORMATION FOR SEQ ID NO: 4:
100    (i) SEQUENCE CHARACTERISTICS:
101        (A) LENGTH: 18 amino acids
102        (B) TYPE: amino acid
103        (C) STRANDEDNESS: unknown
104        (D) TOPOLOGY: unknown
105    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
106    Ser Ile Ser Gln Ala Val His Ala Ala Arg Ala Glu Ile Asn Glu Ala
107    1             5             10             15
108    Gly Arg
109
116 (2) INFORMATION FOR SEQ ID NO: 5:
117    (i) SEQUENCE CHARACTERISTICS:
118        (A) LENGTH: 18 amino acids
119        (B) TYPE: amino acid
120        (C) STRANDEDNESS: unknown
121        (D) TOPOLOGY: unknown
122    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:
123    Ser Ile Ser Gln Ala Val His Ala Ala His Tyr Glu Ile Asn Glu Ala
124    1             5             10             15
125    Gly Arg
126
132 (2) INFORMATION FOR SEQ ID NO: 6:
133    (i) SEQUENCE CHARACTERISTICS:
134        (A) LENGTH: 13 amino acids
135        (B) TYPE: amino acid
136        (C) STRANDEDNESS: unknown
137        (D) TOPOLOGY: unknown
138    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:
139    Asn Leu Cys Asn Ile Pro Cys Ser Ala Leu Leu Ser Ser
140    1             5             10
141
146 (2) INFORMATION FOR SEQ ID NO: 7:
147    (i) SEQUENCE CHARACTERISTICS:

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149      (A) LENGTH: 11 amino acids
150      (B) TYPE: amino acid
151      (C) STRANDEDNESS: unknown
152      (D) TOPOLOGY: unknown
154      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:
156      Gln Ile Ser Val Gln Pro Ala Phe Ser Val Gln
157      1             5             10
160 (2) INFORMATION FOR SEQ ID NO: 8:
162      (i) SEQUENCE CHARACTERISTICS:
163          (A) LENGTH: 13 amino acids
164          (B) TYPE: amino acid
165          (C) STRANDEDNESS: unknown
166          (D) TOPOLOGY: unknown
168      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:
170      Pro Lys Tyr Val Lys Gln Asn Thr Leu Lys Leu Ala Thr
171      1             5             10
174 (2) INFORMATION FOR SEQ ID NO: 9:
176      (i) SEQUENCE CHARACTERISTICS:
177          (A) LENGTH: 13 amino acids
178          (B) TYPE: amino acid
179          (C) STRANDEDNESS: unknown
180          (D) TOPOLOGY: unknown
182      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:
184      His Tyr Gly Ser Leu Pro Gln Lys Ser Gln His Gly Arg
185      1             5             10
188 (2) INFORMATION FOR SEQ ID NO: 10:
190      (i) SEQUENCE CHARACTERISTICS:
191          (A) LENGTH: 13 amino acids
192          (B) TYPE: amino acid
193          (C) STRANDEDNESS: unknown
194          (D) TOPOLOGY: unknown
196      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:
198      His Ser Leu Gly Lys Trp Leu Gly His Pro Asp Lys Phe
199      1             5             10
202 (2) INFORMATION FOR SEQ ID NO: 11:
204      (i) SEQUENCE CHARACTERISTICS:
205          (A) LENGTH: 14 amino acids
206          (B) TYPE: amino acid
207          (C) STRANDEDNESS: unknown
208          (D) TOPOLOGY: unknown
210      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:
212      Met Ala Ser Gln Lys Arg Pro Ser Gln Arg Ser Lys Tyr Leu
213      1             5             10
216 (2) INFORMATION FOR SEQ ID NO: 12:
218      (i) SEQUENCE CHARACTERISTICS:
219          (A) LENGTH: 27 base pairs
220          (B) TYPE: nucleic acid
221          (C) STRANDEDNESS: unknown
222          (D) TOPOLOGY: unknown

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224      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:
226 GCAGAAGAAT TCGAGCTCGG CCCCCAG                                27
229 (2) INFORMATION FOR SEQ ID NO: 13:
231      (i) SEQUENCE CHARACTERISTICS:
232          (A) LENGTH: 33 base pairs
233          (B) TYPE: nucleic acid
234          (C) STRANDEDNESS: unknown
235          (D) TOPOLOGY: unknown
237      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:
239 GATGATATCA GAGAGAAATA CATACTAACA CAC                            33
242 (2) INFORMATION FOR SEQ ID NO: 14:
244      (i) SEQUENCE CHARACTERISTICS:
245          (A) LENGTH: 30 base pairs
246          (B) TYPE: nucleic acid
247          (C) STRANDEDNESS: unknown
248          (D) TOPOLOGY: unknown
250      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:
252 CGGAAGAAAG AGACTTCGGC CGCTACTTAC                                30
255 (2) INFORMATION FOR SEQ ID NO: 15:
257      (i) SEQUENCE CHARACTERISTICS:
258          (A) LENGTH: 47 base pairs
259          (B) TYPE: nucleic acid
260          (C) STRANDEDNESS: unknown
261          (D) TOPOLOGY: unknown
263      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:
265 GTGTGTTAGT ATGTATTTCT CTCTGATATC TTCAGCTTCC AGCAGTG          47
268 (2) INFORMATION FOR SEQ ID NO: 16:
270      (i) SEQUENCE CHARACTERISTICS:
271          (A) LENGTH: 21 base pairs
272          (B) TYPE: nucleic acid
273          (C) STRANDEDNESS: unknown
274          (D) TOPOLOGY: unknown
276      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:
278 TCTTCTAGAA GACCACGCTA C                                          21
281 (2) INFORMATION FOR SEQ ID NO: 17:
283      (i) SEQUENCE CHARACTERISTICS:
284          (A) LENGTH: 36 base pairs
285          (B) TYPE: nucleic acid
286          (C) STRANDEDNESS: unknown
287          (D) TOPOLOGY: unknown
289      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:
291 GATGATATCC GGCCGAAGTC TCTTCTTCC GTTGTC                          36
294 (2) INFORMATION FOR SEQ ID NO: 18:
296      (i) SEQUENCE CHARACTERISTICS:
297          (A) LENGTH: 24 base pairs
298          (B) TYPE: nucleic acid
299          (C) STRANDEDNESS: unknown
300          (D) TOPOLOGY: unknown
302      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

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304 CAGGGTTATC AACACCCTGA AAAC 24
306 (2) INFORMATION FOR SEQ ID NO: 19:
308     (i) SEQUENCE CHARACTERISTICS:
309         (A) LENGTH: 21 base pairs
310         (B) TYPE: nucleic acid
311         (C) STRANDEDNESS: unknown
312         (D) TOPOLOGY: unknown
314     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:
316 GTCACAGTTA TCCACTCTGT C 21
319 (2) INFORMATION FOR SEQ ID NO: 20:
321     (i) SEQUENCE CHARACTERISTICS:
322         (A) LENGTH: 38 base pairs
323         (B) TYPE: nucleic acid
324         (C) STRANDEDNESS: unknown
325         (D) TOPOLOGY: unknown
327     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:
329 CCGTCTCCTC AGGTACGGCC GGCCTCTCCA GGTCTTCG 38
332 (2) INFORMATION FOR SEQ ID NO: 21:
334     (i) SEQUENCE CHARACTERISTICS:
335         (A) LENGTH: 39 base pairs
336         (B) TYPE: nucleic acid
337         (C) STRANDEDNESS: unknown
338         (D) TOPOLOGY: unknown
340     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:
342 CACAGTTATC CACTCTGTCT TTGATATCAC AGGTGTCCT 39
345 (2) INFORMATION FOR SEQ ID NO: 22:
347     (i) SEQUENCE CHARACTERISTICS:
348         (A) LENGTH: 13 amino acids
349         (B) TYPE: amino acid
350         (C) STRANDEDNESS: unknown
351         (D) TOPOLOGY: unknown
353     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:
355     His Ser Leu Gly Lys Tyr Leu Gly His Pro Asp Lys Phe
356     1          5          10
359 (2) INFORMATION FOR SEQ ID NO: 23:
361     (i) SEQUENCE CHARACTERISTICS:
362         (A) LENGTH: 13 amino acids
363         (B) TYPE: amino acid
364         (C) STRANDEDNESS: unknown
365         (D) TOPOLOGY: unknown
367     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:
369     His Ser Leu Gly Lys Leu Leu Gly His Pro Asp Lys Phe
370     1          5          10
373 (2) INFORMATION FOR SEQ ID NO: 24:
375     (i) SEQUENCE CHARACTERISTICS:
376         (A) LENGTH: 18 amino acids
377         (B) TYPE: amino acid
378         (C) STRANDEDNESS: unknown
379         (D) TOPOLOGY: unknown

```

VERIFICATION SUMMARY

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Input Set : N:\Cr3\RULE60\09848164.txt

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L:30 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:31 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:1861 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:122
L:1865 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:122
L:1869 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:122
L:1873 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:122
L:1877 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:122
L:1881 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:122
L:1885 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:122
L:1889 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:122
L:1893 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:122
L:1897 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:122
L:1901 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:122
L:1905 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:122
L:1909 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:122
L:1913 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:122
L:1917 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:122
L:1921 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:122
L:1925 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:122
L:1929 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:122
L:1933 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:122
L:1937 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:122
L:1941 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:122
L:1945 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:122
L:1949 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:122
L:1953 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:122
L:1957 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:122
L:1961 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:122
L:1965 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:122
L:1969 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:122
L:1973 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:122
L:1977 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:122
L:1981 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:122
L:1985 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:122
L:2006 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:123
L:2010 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:123
L:2014 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:123
L:2018 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:123
L:2022 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:123
L:2026 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:123
L:2030 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:123
L:2034 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:123
L:2038 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:123
L:2042 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:123
L:2046 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:123
L:2050 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:123
L:2054 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:123
L:2058 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:123

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L:2062 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:123
L:2066 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:123
L:2070 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:123
L:2074 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:123